



1638

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RAW SEQUENCE LISTING

DATE: 02/05/2002

PATENT APPLICATION: US/09/548,971B

TIME: 14:17:10

Input Set : A:\19452a-7sub.app

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 TECH CENTER 1600/2900

3 <110> APPLICANT: Liljegren, Sarah
 4 Yanofsky, Martin F.
 5 The Regents of the University of California
 7 <120> TITLE OF INVENTION: Control of Fruit Dehiscence in Arabidopsis by
 8 INDEHISCENT1 Genes
 10 <130> FILE REFERENCE: 19452A-000700US
 12 <140> CURRENT APPLICATION NUMBER: US 09/548,971B
 C--> 13 <141> CURRENT FILING DATE: 1996-09-22
 15 <150> PRIOR APPLICATION NUMBER: US 60/090,649
 16 <151> PRIOR FILING DATE: 1998-06-25
 18 <150> PRIOR APPLICATION NUMBER: US 09/339,998
 19 <151> PRIOR FILING DATE: 1999-06-25
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 28 <213> ORGANISM: Arabidopsis thaliana
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141 35 40 45
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148 Met Leu Asp Pro Pro Pro Glu Thr Leu Ile His Leu Asp Glu Asp Glu
149 65 70 75
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152 Glu Tyr Asp Glu Asp Met Asp Ala Met Lys Glu Met Gln Tyr Met Ile
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163 cgt cgg cgt cgg gaa agg atc agc gag aag atc cga att ctc aag agg 3193
164 Arg Arg Arg Arg Glu Arg Ile Ser Glu Lys Ile Arg Ile Leu Lys Arg
165 130 135 140
167 atc gtg cct ggt ggt gcg aag atg gac aca gct tcc atg ctc gac gaa 3241
168 Ile Val Pro Gly Gly Ala Lys Met Asp Thr Ala Ser Met Leu Asp Glu
169 145 150 155
171 gcc ata cgt tac acc aag ttc ttg aaa cgg cag gtg agg att ctt cag 3289
172 Ala Ile Arg Tyr Thr Lys Phe Leu Lys Arg Gln Val Arg Ile Leu Gln
173 160 165 170 175
175 cct cac tct cag att gga gct cct atg gct aac ccc tct tac ctt tgt 3337
176 Pro His Ser Gln Ile Gly Ala Pro Met Ala Asn Pro Ser Tyr Leu Cys
177 180 185 190
179 tat tac cac aac tcc caa ccc tga tgaactacac agaagctcgc tagctagaca 3391
180 Tyr Tyr His Asn Ser Gln Pro
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213 35 40 45
214 Leu Thr Gln Glu His Ala Ala Phe Leu Asn Asp Pro His His Leu Met
215 50 55 60
216 Leu Asp Pro Pro Pro Glu Thr Leu Ile His Leu Asp Glu Asp Glu Glu
217 65 70 75 80
218 Tyr Asp Glu Asp Met Asp Ala Met Lys Glu Met Gln Tyr Met Ile Ala
219 85 90 95
220 Val Met Gln Pro Val Asp Ile Asp Pro Ala Thr Val Pro Lys Pro Asn
221 100 105 110
222 Arg Arg Asn Val Arg Ile Ser Asp Asp Pro Gln Thr Val Val Ala Arg
223 115 120 125

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228 Ile Arg Tyr Thr Lys Phe Leu Lys Arg Gln Val Arg Ile Leu Gln Pro
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257 aacgttgaa aagtcattta tcgtatccag ctcatatttc ctatgctaaga tcaaatcaag 780
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275 ttgatttctt atgtttttta tttatggaat ttaaagacgg attgtttagg tcgtttctct 1860
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280 tattggggaa tcagtatatt agcttgggta actatacttc tggaaatact tgaagattta 2160
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283 ggttggggttc aaaagccttt tcaaaagttc catttttttaa attcaaggac attttacata 2340
284 ggaaataagt tgagtcataa aaaataatgg ttatttttga aggttttttt tttgattaaa 2400
285 acgcacatat taagaagtta gttttttttc actaccaa atcaattaat ttaaaaccat 2460
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289 ataataagag acatgcatgt aagcattcgg ttaattaatc gagtcaaaga tatatatcag 2700
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305 attattattc taagatatat gatgtacaat tgtgtaccaa gtttctttat cttgatatca 180
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307 attgattggt aattagggtt tgatcattct gtatgaaagc tttggcctgc aaattaattt 300
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309 tttgtatcaa ttatctgaat ctgatgagtg taggttatat atggattagc aaaaaagaaa 420
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322 <220> FEATURE:

323 <221> NAME/KEY: modified_base

324 <222> LOCATION: (935)..(941)

325 <223> OTHER INFORMATION: n = any nucleotide

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VERIFICATION SUMMARY

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